

Supplementary Material for

Complex models of sequence evolution require accurate estimators as exemplified with the invariable site plus Gamma model

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Table S1. The 15 TreeBase alignments (5 DNA and 10 protein), where at least one of the three programs PhyML, RAxML or IQ-TREE showed 10% deviation in the estimated $\hat{\alpha}$ and $\widehat{p_{inv}}$ compared with IQ-TREE-EM. Color codes are the same as Figure 1: red (more than 25% deviation from IQ-TREE-EM), yellow (10% to 25% deviation from IQ-TREE-EM) and green (less than 10% deviation from IQ-TREE-EM).

TreeBase ID #seqs x #sites		PhyML	RAxML	IQ-TREE	IQ-TREE-EM
DNA M10243 203 x 1771	$\hat{\alpha}$	0.919	1.338	0.975	0.610
	$\widehat{p_{inv}}$	0.145	0.232	0.163	0.000
	\hat{l}	1.709	1.7025	1.705	1.696
DNA M14164 204 x 5549	$\hat{\alpha}$	0.846	0.930	0.877	0.823
	$\widehat{p_{inv}}$	0.211	0.233	0.222	0.203
	\hat{l}	1.950	1.956	1.949	1.949
DNA M4326 227 x 4055	$\hat{\alpha}$	0.749	0.834	0.651	0.602
	$\widehat{p_{inv}}$	0.516	0.528	0.487	0.470
	\hat{l}	1.669	1.656	1.663	1.653
DNA M8984 201 x 3931	$\hat{\alpha}$	1.002	1.207	1.066	0.961
	$\widehat{p_{inv}}$	0.245	0.286	0.264	0.232
	\hat{l}	0.996	0.997	0.996	0.999
DNA M9143 228 x 1223	$\hat{\alpha}$	0.714	0.834	0.746	0.726
	$\widehat{p_{inv}}$	0.197	0.238	0.220	0.205
	\hat{l}	1.362	1.362	1.378	1.375
Prot M10273 169 x 11009	$\hat{\alpha}$	1.010	0.846	1.014	1.015
	$\widehat{p_{inv}}$	0.156	0.093	0.157	0.157
	\hat{l}	14.892	14.759	14.925	14.927
Prot M1118 137 x 348	$\hat{\alpha}$	0.792	0.697	0.793	0.803
	$\widehat{p_{inv}}$	0.054	0.000	0.060	0.060
	\hat{l}	12.974	13.198	13.652	13.382
Prot M3113 77 x 9918	$\hat{\alpha}$	0.896	0.776	0.895	0.894
	$\widehat{p_{inv}}$	0.050	0.000	0.050	0.049
	\hat{l}	26.403	26.269	26.338	26.304
Prot M3114 77 x 11234	$\hat{\alpha}$	0.920	0.749	0.915	0.915
	$\widehat{p_{inv}}$	0.065	0.000	0.064	0.064
	\hat{l}	27.257	26.788	27.165	27.161

Prot M4539	$\hat{\alpha}$	0.834	0.615	0.831	0.832
59 x 12428	$\widehat{p_{inv}}$	0.135	0.0001	0.135	0.135
		14.780	14.917	14.853	14.847
Prot M4884	$\hat{\alpha}$	0.742	0.493	0.740	0.742
		0.183	0.0001	0.182	0.183
		6.770	6.829	6.783	6.784
Prot M5379	$\widehat{p_{inv}}$	0.922	0.6334	0.922	0.922
		0.154	0.0001	0.154	0.154
		11.215	11.376	11.248	11.249
Prot M7078	$\widehat{p_{inv}}$	0.807	0.508	0.807	0.807
		0.212	0.0001	0.211	0.211
		9.522	9.812	9.516	9.516
Prot M7729	$\widehat{p_{inv}}$	0.751	0.534	0.751	0.752
		0.189	0.021	0.190	0.191
		17.168	18.964	17.425	17.437
Prot M8175	$\widehat{p_{inv}}$	1.098	0.830	1.091	1.093
		0.077	0.0001	0.077	0.078
		11.839	11.806	11.945	11.947

